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## SEQUENCE LISTING

&lt;110&gt; Degussa AG

5 &lt;120&gt; Mutants for the preparation of D-amino acids

&lt;130&gt; 020453 AM

&lt;140&gt;

10 &lt;141&gt;

&lt;160&gt; 8

&lt;170&gt; PatentIn Ver. 2.1

15

&lt;210&gt; 1

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Arthrobacter crystallopoietes

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(948)

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30 agt tcg gaa tca aga ccc gaa gtc gtc gcc cgc ttg att gcc ctg ctg	96
Ser Ser Glu Ser Arg Pro Glu Val Val Ala Arg Leu Ile Ala Leu Leu	
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35 gaa gaa gca gct tcc cag ggc gcg gaa ctg gtg gtc ttt ccc gaa ctc	144
Glu Glu Ala Ala Ser Gln Gly Ala Glu Leu Val Val Phe Pro Glu Leu	
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40 acg ctg acc acg ttc ttc ccg cgt acc tgg ttc gaa gaa ggc gac ttc	192
Thr Leu Thr Thr Phe Phe Pro Arg Thr Trp Phe Glu Glu Gly Asp Phe	
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45 gag gaa tac ttc gat aaa tcc atg ccc aat gac gac gtc gcg ccc ctt	240
Glu Glu Tyr Phe Asp Lys Ser Met Pro Asn Asp Asp Val Ala Pro Leu	
65 70 75 80	

50 ttc gaa cgc gcc aaa gac ctt ggc gtg ggc ttc tac ctc gga tac gcg	288
Phe Glu Arg Ala Lys Asp Leu Gly Val Gly Phe Tyr Leu Gly Tyr Ala	
85 90 95	

55 gaa ctg acc agt gat gag aag cgg tac aac aca tca att ctg gtg aac	336
Glu Leu Thr Ser Asp Glu Lys Arg Tyr Asn Thr Ser Ile Leu Val Asn	
100 105 110	

55 aag cac ggc gac atc gtc ggc aag tac cgc aag atg cat ctg ccg ggc	384
Lys His Gly Asp Ile Val Gly Lys Tyr Arg Lys Met His Leu Pro Gly	
115 120 125	

cac gcc gat aac cgg gaa gga cta ccc aac cag cac ctt gaa aag aaa	432
His Ala Asp Asn Arg Glu Gly Leu Pro Asn Gln His Leu Glu Lys Lys	

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	130	135	140	
	tac ttc cgc gaa gga gat ctc gga ttc ggt gtc ttc gac ttc cac ggc			480
5	Tyr Phe Arg Glu Gly Asp Leu Gly Phe Gly Val Phe Asp Phe His Gly			
	145	150	155	160
	gtg cag gtc gga atg tgt ctc tgc aac gac cgg cga tgg ccg gag gtc			528
	Val Gln Val Gly Met Cys Leu Cys Asn Asp Arg Arg Trp Pro Glu Val			
		165	170	175
10	tac cgc tct ttg gcc ctg cag gga gca gag ctc gtc gtc ctg ggc tac			576
	Tyr Arg Ser Leu Ala Leu Gln Gly Ala Glu Leu Val Val Leu Gly Tyr			
		180	185	190
15	aac acc ccc gat ttc gtt ccc ggc tgg cag gaa gag cct cac gcg aag			624
	Asn Thr Pro Asp Phe Val Pro Gly Trp Gln Glu Glu Pro His Ala Lys			
		195	200	205
20	atg ttc acg cac ctt ctt tca ctt cag gca ggg gca tac cag aac tcg			672
	Met Phe Thr His Leu Leu Ser Leu Gln Ala Gly Ala Tyr Gln Asn Ser			
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	gta ttt gtg gcg gct gcc ggc aag tcg ggc ttc gaa gac ggg cac cac			720
	Val Phe Val Ala Ala Ala Gly Lys Ser Gly Phe Glu Asp Gly His His			
25	225	230	235	240
	atg atc ggc gga tca gcg gtc gcc gcg ccc agc ggc gaa atc ctg gca			768
	Met Ile Gly Gly Ser Ala Val Ala Ala Pro Ser Gly Glu Ile Leu Ala			
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30	aaa gca gcc ggc gag ggc gat gaa gtc gtc gtt gtg aaa gca gac atc			816
	Lys Ala Ala Gly Glu Gly Asp Glu Val Val Val Lys Ala Asp Ile			
		260	265	270
35	gac atg ggc aag ccc tat aag gaa agc gtc ttc gac ttc gcc gcc cat			864
	Asp Met Gly Lys Pro Tyr Lys Glu Ser Val Phe Asp Phe Ala Ala His			
		275	280	285
40	cgg cgc ccc gac gca tac ggc atc atc gcc gaa agg aaa ggg cgg ggc			912
	Arg Arg Pro Asp Ala Tyr Gly Ile Ile Ala Glu Arg Lys Gly Arg Gly			
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Glu Glu Ala Ala Ser Gln Gly Ala Glu Leu Val Val Phe Pro Glu Leu  
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 5 Thr Leu Thr Thr Phe Phe Pro Arg Thr Trp Phe Glu Glu Gly Asp Phe  
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 Glu Glu Tyr Phe Asp Lys Ser Met Pro Asn Asp Asp Val Ala Pro Leu  
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 10 Phe Glu Arg Ala Lys Asp Leu Gly Val Gly Phe Tyr Leu Gly Tyr Ala  
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 Glu Leu Thr Ser Asp Glu Lys Arg Tyr Asn Thr Ser Ile Leu Val Asn  
                                   100                                  105                                  110  
 15 Lys His Gly Asp Ile Val Gly Lys Tyr Arg Lys Met His Leu Pro Gly  
                   115                                  120                                  125  
 His Ala Asp Asn Arg Glu Gly Leu Pro Asn Gln His Leu Glu Lys Lys  
           130                                  135                                  140  
 Tyr Phe Arg Glu Gly Asp Leu Gly Phe Gly Val Phe Asp Phe His Gly  
           145                                  150                                  155                                  160  
 25 Val Gln Val Gly Met Cys Leu Cys Asn Asp Arg Arg Trp Pro Glu Val  
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 Tyr Arg Ser Leu Ala Leu Gln Gly Ala Glu Leu Val Val Leu Gly Tyr  
                                   180                                  185                                  190  
 30 Asn Thr Pro Asp Phe Val Pro Gly Trp Gln Glu Glu Pro His Ala Lys  
                                   195                                  200                                  205  
 Met Phe Thr His Leu Leu Ser Leu Gln Ala Gly Ala Tyr Gln Asn Ser  
           210                                  215                                  220  
 Val Phe Val Ala Ala Ala Gly Lys Ser Gly Phe Glu Asp Gly His His  
           225                                  230                                  235                                  240  
 40 Met Ile Gly Gly Ser Ala Val Ala Ala Pro Ser Gly Glu Ile Leu Ala  
                                   245                                  250                                  255  
 Lys Ala Ala Gly Glu Gly Asp Glu Val Val Val Val Lys Ala Asp Ile  
                                   260                                  265                                  270  
 45 Asp Met Gly Lys Pro Tyr Lys Glu Ser Val Phe Asp Phe Ala Ala His  
                   275                                  280                                  285  
 Arg Arg Pro Asp Ala Tyr Gly Ile Ile Ala Glu Arg Lys Gly Arg Gly  
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10

aaa atc cga gcc gac gtg ctg att gaa aac ggc aaa gtc gcc gct gtc 96  
 Lys Ile Arg Ala Asp Val Leu Ile Glu Asn Gly Lys Val Ala Ala Val  
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15

ggc atg ctg gac gcc gcg acg ccg gac aca gtt gag cgg gtt gac tgc 144  
 Gly Met Leu Asp Ala Ala Thr Pro Asp Thr Val Glu Arg Val Asp Cys  
 35 40 45

20

gac ggc aaa tac gtc atg ccc ggc ggt atc gac gtt cac acc cac atc 192  
 Asp Gly Lys Tyr Val Met Pro Gly Gly Ile Asp Val His Thr His Ile  
 50 55 60

25

gac tcc ccc ctc atg ggg acc acc acc gcc gat gat ttt gtc agc gga 240  
 Asp Ser Pro Leu Met Gly Thr Thr Thr Ala Asp Asp Phe Val Ser Gly  
 65 70 75 80

30

acg att gca gcc gct acc ggc gga aca acg acc atc gtc gat ttc gga 288  
 Thr Ile Ala Ala Ala Thr Gly Gly Thr Thr Thr Ile Val Asp Phe Gly  
 85 90 95

35

cag cag ctc gcc ggc aag aac ctg ctg gaa tcc gca gac gcg cac cac 336  
 Gln Gln Leu Ala Gly Lys Asn Leu Leu Glu Ser Ala Asp Ala His His  
 100 105 110

40

aaa aag gcg cag ggg aaa tcc gtc att gat tac ggc ttc cat atg tgc 384  
 Lys Lys Ala Gln Gly Lys Ser Val Ile Asp Tyr Gly Phe His Met Cys  
 115 120 125

45

gtg acg aac ctc tat gac aat ttc gat tcc cat atg gca gaa ctg aca 432  
 Val Thr Asn Leu Tyr Asp Asn Phe Asp Ser His Met Ala Glu Leu Thr  
 130 135 140

50

cag gac gga atc tcc agt ttc aag gtc ttc atg gcc tac cgc gga agc 480  
 Gln Asp Gly Ile Ser Ser Phe Lys Val Phe Met Ala Tyr Arg Gly Ser  
 145 150 155 160

55

ctg atg atc aac gac ggc gaa ctg ttc gac atc ctc aag gga gtc ggc 528  
 Leu Met Ile Asn Asp Gly Glu Leu Phe Asp Ile Leu Lys Gly Val Gly  
 165 170 175

60

tcc agc ggt gcc aaa cta tgc gtc cac gca gag aac ggc gac gtc atc 576  
 Ser Ser Gly Ala Lys Leu Cys Val His Ala Glu Asn Gly Asp Val Ile  
 180 185 190

65

gac agg atc gcc gcc gac ctc tac gcc caa gga aaa acc ggg ccc ggg 624  
 Asp Arg Ile Ala Ala Asp Leu Tyr Ala Gln Gly Lys Thr Gly Pro Gly  
 195 200 205

70

acc cac gag atc gca cgc ccg ccg gaa tcg gaa gtc gaa gca gtc agc 672

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	225					230					235					240	
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	His	Leu	Ser	Thr	Gln	Gly	Ala	Val	Glu	Glu	Val	Ala	Ala	Ala	Gln	Met	
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15	aca	gga	tgg	cca	atc	agc	gcc	gaa	acg	tgc	acc	cac	tac	ctg	tcg	ctg	816
	Thr	Gly	Trp	Pro	Ile	Ser	Ala	Glu	Thr	Cys	Thr	His	Tyr	Leu	Ser	Leu	
				260					265					270			
20	agc	cgg	gac	atc	tac	gac	cag	ccg	gga	ttc	gag	ccg	gcc	aaa	gct	gtc	864
	Ser	Arg	Asp	Ile	Tyr	Asp	Gln	Pro	Gly	Phe	Glu	Pro	Ala	Lys	Ala	Val	
			275					280					285				
25	ctc	aca	cca	ccg	ctg	cgc	aca	cag	gaa	cac	cag	gac	gcg	ttg	tgg	aga	912
	Leu	Thr	Pro	Pro	Leu	Arg	Thr	Gln	Glu	His	Gln	Asp	Ala	Leu	Trp	Arg	
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30	ggc	att	aac	acc	ggt	gcg	ctc	agc	gtc	gtc	agt	tcc	gac	cac	tgc	ccc	960
	Gly	Ile	Asn	Thr	Gly	Ala	Leu	Ser	Val	Val	Ser	Ser	Asp	His	Cys	Pro	
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35	ttc	tgc	ttt	gag	gaa	aag	cag	cgg	atg	ggg	gca	gat	gac	ttc	cgg	cag	1008
	Phe	Cys	Phe	Glu	Glu	Lys	Gln	Arg	Met	Gly	Ala	Asp	Asp	Phe	Arg	Gln	
					325					330					335		
40	atc	ccc	aac	ggc	ggg	ccc	ggc	gtg	gag	cac	cga	atg	ctc	gtg	atg	tat	1056
	Ile	Pro	Asn	Gly	Gly	Pro	Gly	Val	Glu	His	Arg	Met	Leu	Val	Met	Tyr	
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45	gag	acc	ggt	gtc	gcg	gaa	gga	aaa	atg	acg	atc	gag	aaa	ttc	gtc	gag	1104
	Glu	Thr	Gly	Val	Ala	Glu	Gly	Lys	Met	Thr	Ile	Glu	Lys	Phe	Val	Glu	
			355				360						365				
50	gtg	act	gcc	gag	aac	ccg	gcc	aag	caa	ttc	gat	atg	tac	ccg	aaa	aag	1152
	Val	Thr	Ala	Glu	Asn	Pro	Ala	Lys	Gln	Phe	Asp	Met	Tyr	Pro	Lys	Lys	
			370				375					380					
55	gga	aca	att	gca	ccg	ggc	tcc	gat	gca	gac	atc	atc	gtg	gtc	gac	ccc	1200
	Gly	Thr	Ile	Ala	Pro	Gly	Ser	Asp	Ala	Asp	Ile	Ile	Val	Val	Asp	Pro	
	385					390					395					400	
60	aac	gga	aca	acc	ctc	atc	agt	gcc	gac	acc	caa	aaa	caa	aac	atg	gac	1248
	Asn	Gly	Thr	Thr	Leu	Ile	Ser	Ala	Asp	Thr	Gln	Lys	Gln	Asn	Met	Asp	
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65	tac	acg	ctg	ttc	gaa	ggc	ttc	aaa	atc	cgt	tgc	tcc	atc	gac	cag	gtg	1296
	Tyr	Thr	Leu	Phe	Glu	Gly	Phe	Lys	Ile	Arg	Cys	Ser	Ile	Asp	Gln	Val	
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70	ttc	tcg	cgt	ggc	gac	ctg	atc	agc	gtc	aaa	ggc	gaa	tat	gtc	ggc	acc	1344
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cgc ggc cgc ggc gaa ttc atc aag cgg agc gct tgg agc cac ccg cag      1392
Arg Gly Arg Gly Glu Phe Ile Lys Arg Ser Ala Trp Ser His Pro Gln
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    <213> Arthrobacter crystallopoietes

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   Gly Met Leu Asp Ala Ala Thr Pro Asp Thr Val Glu Arg Val Asp Cys
      35              40              45

25 Asp Gly Lys Tyr Val Met Pro Gly Gly Ile Asp Val His Thr His Ile
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   Asp Ser Pro Leu Met Gly Thr Thr Thr Ala Asp Asp Phe Val Ser Gly
      65              70              75              80

30 Thr Ile Ala Ala Ala Thr Gly Gly Thr Thr Thr Ile Val Asp Phe Gly
      85              90              95

   Gln Gln Leu Ala Gly Lys Asn Leu Leu Glu Ser Ala Asp Ala His His
      100              105              110

35 Lys Lys Ala Gln Gly Lys Ser Val Ile Asp Tyr Gly Phe His Met Cys
      115              120              125

40 Val Thr Asn Leu Tyr Asp Asn Phe Asp Ser His Met Ala Glu Leu Thr
      130              135              140

   Gln Asp Gly Ile Ser Ser Phe Lys Val Phe Met Ala Tyr Arg Gly Ser
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45 Leu Met Ile Asn Asp Gly Glu Leu Phe Asp Ile Leu Lys Gly Val Gly
      165              170              175

   Ser Ser Gly Ala Lys Leu Cys Val His Ala Glu Asn Gly Asp Val Ile
      180              185              190

50 Asp Arg Ile Ala Ala Asp Leu Tyr Ala Gln Gly Lys Thr Gly Pro Gly
      195              200              205

55 Thr His Glu Ile Ala Arg Pro Pro Glu Ser Glu Val Glu Ala Val Ser
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   Arg Ala Ile Lys Ile Ser Arg Met Ala Glu Val Pro Leu Tyr Phe Val
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His Leu Ser Thr Gln Gly Ala Val Glu Glu Val Ala Ala Ala Gln Met  
 245 250 255  
 5 Thr Gly Trp Pro Ile Ser Ala Glu Thr Cys Thr His Tyr Leu Ser Leu  
 260 265 270  
 Ser Arg Asp Ile Tyr Asp Gln Pro Gly Phe Glu Pro Ala Lys Ala Val  
 275 280 285  
 10 Leu Thr Pro Pro Leu Arg Thr Gln Glu His Gln Asp Ala Leu Trp Arg  
 290 295 300  
 15 Gly Ile Asn Thr Gly Ala Leu Ser Val Val Ser Ser Asp His Cys Pro  
 305 310 315 320  
 Phe Cys Phe Glu Glu Lys Gln Arg Met Gly Ala Asp Asp Phe Arg Gln  
 325 330 335  
 20 Ile Pro Asn Gly Gly Pro Gly Val Glu His Arg Met Leu Val Met Tyr  
 340 345 350  
 Glu Thr Gly Val Ala Glu Gly Lys Met Thr Ile Glu Lys Phe Val Glu  
 355 360 365  
 25 Val Thr Ala Glu Asn Pro Ala Lys Gln Phe Asp Met Tyr Pro Lys Lys  
 370 375 380  
 30 Gly Thr Ile Ala Pro Gly Ser Asp Ala Asp Ile Ile Val Val Asp Pro  
 385 390 395 400  
 Asn Gly Thr Thr Leu Ile Ser Ala Asp Thr Gln Lys Gln Asn Met Asp  
 405 410 415  
 35 Tyr Thr Leu Phe Glu Gly Phe Lys Ile Arg Cys Ser Ile Asp Gln Val  
 420 425 430  
 Phe Ser Arg Gly Asp Leu Ile Ser Val Lys Gly Glu Tyr Val Gly Thr  
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25 gagctgcttc 70

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40 gccatggtcc 70